



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: de la Monte, Suzanne
Wands, Jack R.
- (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention
of Alzheimer's Disease
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
 - (B) STREET: 1100 New York Ave., Suite 600
 - (C) CITY: Washington
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Esmond, Robert W.
 - (B) REGISTRATION NUMBER: 32,893
 - (C) REFERENCE/DOCKET NUMBER: 0609.4370000
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-371-2600
 - (B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 15..1139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT TGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC
Met Glu Phe Ser Leu Leu Pro Arg Leu Glu Cys
1 5 10

AAT Asn	GGC Gly	GCA Ala	ATC Ile	TCA Ser	GCT Ala	CAC His	CGC Arg	AAC Asn	CTC Leu	CGC Arg	CTC Leu	CCG Pro	GGT Gly	TCA Ser	AGC Ser	98
	15						20					25				
GAT Asp	TCT Ser	CCT Pro	GCC Ala	TCA Ser	GCC Ala	TCC Ser	CCA Pro	GTA Val	GCT Ala	GGG Gly	ATT Ile	ACA Thr	GGC Gly	ATG Met	TGC Cys	146
	30					35					40					
ACC Thr	CAC His	GCT Ala	CGG Arg	CTA Leu	ATT Ile	TTG Leu	TAT Tyr	TTT Phe	TTT Phe	TTA Leu	GTA Val	GAG Glu	ATG Met	GAG Glu	TTT Phe	194
	45				50					55					60	
CTC Leu	CAT His	GTT Val	GGT Gly	CAG Gln	GCT Ala	GGT Gly	CTC Leu	GAA Glu	CTC Leu	CCG Pro	ACC Thr	TCA Ser	GAT Asp	GAT Asp	CCC Pro	242
				65				70					75			
TCC Ser	GTC Val	TCG Ser	GCC Ala	TCC Ser	CAA Gln	AGT Ser	GCT Ala	AGA Arg	TAC Tyr	AGG Arg	ACT Thr	GGC Gly	CAC His	CAT His	GCC Ala	290
			80					85					90			
CGG Arg	CTC Leu	TGC Cys	CTG Leu	GCT Ala	AAT Asn	TTT Phe	TGT Cys	GGT Gly	AGA Arg	AAC Asn	AGG Arg	GTT Ser	TCA Ser	CTG Leu	ATG Met	338
		95					100					105				
TGC Cys	CCA Leu	AGC Ser	TGG Trp	TCT Ser	CCT Pro	GAG Leu	CTC Leu	AAG Lys	CAG Gln	TCC Ser	ACC Thr	TGC Cys	CTC Leu	AGC Ser	CTC Leu	386
	110					115					120					
CCA Pro	AAG Lys	TGC Cys	TGG Trp	GAT Asp	TAC Tyr	AGG Arg	CGT Arg	GCA Ala	GCC Ala	GTG Ala	CCT Pro	GGC Gly	CTT Leu	TTT Phe	ATT Ile	434
	125				130					135					140	
TTA Leu	TTT Phe	TTT Phe	TTA Leu	AGA Arg	CAC His	AGG Arg	TGT Cys	CCC Pro	ACT Thr	CTT Leu	ACC Thr	CAG Gln	GAT Asp	GAA Glu	GTG Val	482
				145				150						155		
CAG Gln	TGG Trp	TGT Cys	GAT Asp	CAC His	AGC Ser	TCA Ser	CTG Leu	CAG Gln	CCT Pro	TCA Ser	ACT Thr	CCT Pro	GAG Glu	ATC Ile	AAG Lys	530
			160					165					170			
CAT His	CCT Pro	CCT Pro	GCC Ala	TCA Ser	GCC Ala	TCC Ser	CAA Gln	GTA Val	GCT Ala	GGG Gly	ACC Thr	AAA Lys	GAC Asp	ATG Met	CAC His	578
		175					180					185				
CAC His	TAC Tyr	ACC Thr	TGG Trp	CTA Leu	ATT Ile	TTT Phe	ATT Ile	TTT Phe	ATT Ile	TTT Phe	AAT Asn	TTT Phe	TTG Leu	AGA Arg	CAG Gln	626
	190				195						200					
AGT Ser	CTC Leu	AAC Asn	TCT Ser	GTC Val	ACC Thr	CAG Gln	GCT Ala	GGA Gly	GTG Val	CAG Gln	TGG Trp	CGC Arg	AAT Asn	CTT Leu	GGC Gly	674
	205				210					215					220	
TCA Ser	CTG Leu	CAA Gln	CCT Pro	CTG Pro	CCT Pro	CCC Gly	GGG Phe	TTC Lys	AAG Lys	TTA Leu	TTC Phe	TCC Ser	TGC Cys	CCC Pro	AGC Ser	722
			225					230						235		
CTC Leu	CTG Leu	AGT Ser	AGC Ser	TGG Trp	GAC Asp	TAC Tyr	AGG Arg	CGC Arg	CCA Pro	CCA Pro	CGC Arg	CTA Leu	GCT Ala	AAT Asn	TTT Phe	770
			240					245					250			
TTT Phe	GTA Val	TTT Phe	TTA Leu	GTA Val	GAG Glu	ATG Met	GGG Gly	TTC Phe	ACC Thr	ATG Met	TTC Phe	GCC Ala	AGG Arg	TTG Leu	ATC Ile	818
	255						260					265				
TTG ATC	ATC TCT	TCT GGA	CCT TGT	GAT CTG	CCT GCC	TCG GCC	TCC CAA	AGT GCT								866

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|
| 85 | | | | | | | | | | 90 | | | | | 95 | | | | | |
| Ala | Asn | Phe | Cys | Gly | Arg | Asn | Arg | Val | Ser | Leu | Met | Cys | Pro | Ser | Trp | | | | | |
| | | | 100 | | | | | | | | | | | | | | | | | |
| Ser | Pro | Glu | Leu | Lys | Gln | Ser | Thr | Cys | Leu | Ser | Leu | Pro | Lys | Cys | Trp | | | | | |
| | | | 115 | | | | | | | | | | | | | | | | | |
| Asp | Tyr | Arg | Arg | Ala | Ala | Val | Pro | Gly | Leu | Phe | Ile | Leu | Phe | Phe | Leu | | | | | |
| | | | 130 | | | | 135 | | | | | | | | | | | | | |
| Arg | His | Arg | Cys | Pro | Thr | Leu | Gln | Asp | Glu | Val | Gln | Trp | Cys | Asp | | | | | | |
| | | | 145 | | | | 150 | | | | 155 | | | | | | | | | |
| His | Ser | Ser | Leu | Gln | Pro | Ser | Thr | Pro | Glu | Ile | Lys | His | Pro | Pro | Ala | | | | | |
| | | | | 165 | | | | | | | | | | | | | | | | |
| Ser | Ala | Ser | Gln | Val | Ala | Gly | Thr | Lys | Asp | Met | His | His | Tyr | Thr | Trp | | | | | |
| | | | 180 | | | | | | | | | | | | | | | | | |
| Leu | Ile | Phe | Ile | Phe | Ile | Phe | Asn | Phe | Leu | Arg | Gln | Ser | Leu | Asn | Ser | | | | | |
| | | | 195 | | | | 200 | | | | 205 | | | | | | | | | |
| Val | Thr | Gln | Ala | Gly | Val | Gln | Trp | Arg | Asn | Leu | Gly | Ser | Leu | Gln | Pro | | | | | |
| | | | 210 | | | | 215 | | | | 220 | | | | | | | | | |
| Leu | Pro | Pro | Gly | Phe | Lys | Leu | Phe | Ser | Cys | Pro | Ser | Leu | Leu | Ser | Ser | | | | | |
| | | | 225 | | | | 230 | | | | 235 | | | | | | | | | |
| Trp | Asp | Tyr | Arg | Arg | Pro | Pro | Arg | Leu | Ala | Asn | Phe | Phe | Val | Phe | Leu | | | | | |
| | | | | 245 | | | | | | | | | | | | | | | | |
| Val | Glu | Met | Gly | Phe | Thr | Met | Phe | Ala | Arg | Leu | Ile | Leu | Ile | Ser | Gly | | | | | |
| | | | 260 | | | | 265 | | | | 270 | | | | | | | | | |
| Pro | Cys | Asp | Leu | Pro | Ala | Ser | Ala | Ser | Gln | Ser | Ala | Gly | Ile | Thr | Gly | | | | | |
| | | | 275 | | | | 280 | | | | 285 | | | | | | | | | |
| Val | Ser | His | His | Ala | Arg | Leu | Ile | Phe | Asn | Phe | Cys | Leu | Phe | Glu | Met | | | | | |
| | | | 290 | | | | 295 | | | | 300 | | | | | | | | | |
| Glu | Ser | His | Ser | Val | Thr | Gln | Ala | Gly | Val | Gln | Trp | Pro | Asn | Leu | Gly | | | | | |
| | | | 305 | | | | 310 | | | | 315 | | | | | | | | | |
| Ser | Leu | Gln | Pro | Leu | Pro | Pro | Gly | Leu | Lys | Arg | Phe | Ser | Cys | Leu | Ser | | | | | |
| | | | | 325 | | | | | | | | | | | | | | | | |
| Leu | Pro | Ser | Ser | Trp | Asp | Tyr | Gly | His | Leu | Pro | Pro | His | Pro | Ala | Asn | | | | | |
| | | | 340 | | | | 345 | | | | 350 | | | | | | | | | |
| Phe | Cys | Ile | Phe | Ile | Arg | Gly | Gly | Val | Ser | Pro | Tyr | Leu | Ser | Gly | Trp | | | | | |
| | | | 355 | | | | 360 | | | | 365 | | | | | | | | | |
| Ser | Gln | Thr | Pro | Asp | Leu | Arg | | | | | | | | | | | | | | |
| | | | 370 | | | | 375 | | | | | | | | | | | | | |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTTTTTT GAGATGGAGT TTTGCTCTT GTTGCCGAGG CTGGAGTGCA ATGGCGCAAT	60
CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC	120
AGTAGCTGGG ATTACAGGCA TGTGCACCAC GCTCGGCTAA TTTTGTATTT TTTTITAGTA	180
GAGATGGAGT TTAACCTCAT GTTGGTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC	240
TCCCGTCTCG GCCTGCCCAA AGTGCTGAGA TTACAGGCAT GAGCCACCAT GCCCGGCCTC	300
TGCCCTGGCTA ATTTTGTGG TAGAAACAGG GTTTCAGTGA TGTTGCCCAA GCTGGTCTCC	360
TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GCGCTCAGCC	420
GTGCTGGCC TTTTATTTTT ATTTTTTTTA AGACACAGGT GTACCACTCT TACCCAGGAT	480
GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTTCAA CTCCTGAGAT CAAGCAATCC	540
TCCTGCCTCA GCCTCCCAA TAGCTGGGAC CAAAGACATG CACCACTACA CCTGGTAATT	600
TTTATTTTTA TTTTAAATTT TTTGAGACAG AGTCTCACTC TGTCACCCAG GCTGGAGTGC	660
AGTGGCGCAA TCTTGGCTCA CTGCAACCTC TGCCCTCCGG GTTCAAGTTA TTCTCTGCC	720
CCAGCTCCT GAGTAGCTGG GACTACAGGC GCCCACCACG CCTAGTAAT TTTTTGTAT	780
TTTATAGTAG GATGGGGTTT CACCATGTTT GCCAGTTGA TCTTGATCTC TTGACCTTGT	840
GATCTGCCTG CCTCGGCCTA CCCAAAGTGC TGGGATTACA GGTCGTGACT CCACGCCGGC	900
CTATTTTTAA TTTTGTTTG TTTGAAATGG AATCTCACTC TGTTACCCAG GTCGGAGTGC	960
AATGGCAAAT CTCGCTACT CGCAACCTCT GCCTCCCGGG TCAAGCGATT CTCCTGTCTC	1020
AGCCTCCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCCGCTAATT TTTGTATTTT	1080
CATTAGAGGC GGGTTTACCA TATTTGTCAG GCTGGGTCTC AAACCTCTGA CCTCAGGTGA	1140
CCCACCTGCC TCAGCCTTCC AAAGTGCTGG GATTACAGGC GTGAGCCACC TCACCCAGCC	1200
GGCTAATTTG GAATAAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC	1260
TCAAACCTCT GCCTTCAGTC AATCCTTCCA AATGAGCCAC AACACCCAGC CAGTCACATT	1320
TTTAAACAG TTACATCTTT ATTTTAGTAT ACTAGAAAGT AATACAATAA ACATGTCAAA	1381

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTTTTTTTT GAGATGGAGT TTTGCTCTT GTTGCCCGAG CTGGAGTGCA ATGGCGCAAT	60
CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC	120
AGTAGGCTGG GATTACAGGC ATGTGCACCA CGCTCGGCTA ATTTGTATT TTTTTTAGT	180
AGAGATGGAG TTCTCCATG TTGGTCAGGC TGGTCTCGAA CTCGCACCTC AGATGATCCT	240
CCCCTCTCGG CCTCCCAAAG TGCTAGATAC AGGACTGAGC ACCATGCCCC GCCTCTGCCT	300
GGCTAATTTT TGTGGTAGAA ACAGGGTTTC ACTGATGTGC CCAAGCTGGT CTCCTGAGCT	360
CAAGCAGTCC ACCTGCCTCA GCCTCCCAA GTGCTGGGAT TACAGGCGTG CAGCCGTGCC	420
TGGCCTTTTT ATTTTATTTT TTTTAAGACA CAGGTGTCCC ACTCTTACCC AGGATGAAGT	480
GCAGTGGTGT GATCACAGCT CACTGCAGCC TTCAACTCTG AGATCAAGCA TCCTCCTGCC	540
TCAGCCTCCC AAAGTAGCTG GGACCAAAGA CATGCACCAC TACACCTGGC TAATTTTAT	600
TTTATTTTTT AATTTTTTGA GACAGAGTCT CAACTCTGTC ACCCAGGCTG GAGTGACATG	660
GCGCAATCTT GGCTCACTGC AACCTCTGCC TCCCGGGTTC AAGTTATCTT CTGCCCCAG	720
CCTCCTGAGT AGCTGGGACT ACAGGCGCCC ACCACGCCTA GCTAATTTTT TTGATTTTTT	780
AGTAGAGATG GGGTTTCACC ATGTTCCGCA GGTGTATGCT AGATCTCTTG ACCTTGATGAT	840
CTGCCTGCCT CGGCCTCCCA AAGTGCTGGG ATTACAGGAC GTGACGCCCA CCGCCCGGCC	900
TATTTTTAAT TTTTGTGTTG TTGAAATGGA ATCTCACTCT GTTACCCAGG CTGGAGTGCA	960
ATGGCCAAAT CTCGGCTCAC TGCAACCTCT GCCTCCCGGG CTCAAGCGAT TCTCTGTCT	1020
CAGCCTCCCA AGCAGCTGGG ATTACGGGCA CCTGCACCAC ACCCCGCTAA TTTTGTATT	1080
TTCATTAGAG GCGGGGTTTC ACCATATTTG TCAGGCTGGT CTCAAATCC TGACCTCAGG	1140
TGACCCACCT GCCTCAGCCT TCCAAAGTGC TGGGATTACA GCGGTGACGC CTCACCCAGC	1200
CGGCTAATTT AGATAAAAAA ATATGTAGCA ATGGGGGGTC TTGCTATGTT GCCCAGGCTG	1260
GTCTCAAATC TCTGGCTTCA TGCAATCCTT CCAAATGAGC CACAACACC AGCCAGTCAC	1320
ATTTTAAAC AGTTACATCT TTATTTTAGT ATACTAGAAA GTGATACGAT AACATGGCGG	1380
AACCTGCAAA TTCGAGTAGT ACAGAGTCTT TTATAACT	1418

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGTCCCACTC TTACCCAGGA TG

22

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGCAGGCAG ATCACAAGGT CCAG

24

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATGGATGAC GATATCGCTG

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAGGTAGT CTGTCAGGT

19

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCATCCTGG GTAAGAGTGG GACACCTGTG

30

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGTGCATGT CTTTGGTCCC AGCTAC

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCAACCTGG CGAACATGGT GAACCCCATC

30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACTGCACTT NCCA

14

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCAGGTGTAG NCCA

14

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAAGGTCCAG NCCA

14